

CT Check Tags: Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Amino Acid Sequence

Arginine

Bacteriophages

Base Sequence

Circular Dichroism

Conserved Sequence

\*Cytochrome b: BI, biosynthesis

\*Cytochrome b: CH, chemistry

Databases, Factual

Enzyme-Linked Immunosorbent Assay

Genetic Vectors

Hemerythrin: AA, analogs & derivatives

Hemerythrin: BI, biosynthesis

Hemerythrin: CH, chemistry

Models, Structural

Molecular Sequence Data

Mutagenesis, Site-Directed

Oligodeoxyribonucleotides

Protein Folding

\*Protein Structure, Secondary

Proteins: BI, biosynthesis

\*Proteins: CH, chemistry

Random Allocation

Recombinant Proteins: BI, biosynthesis

Recombinant Proteins: CH, chemistry

Serine

Serum Albumin, Bovine

Tryptophan

RN 56-45-1 (Serine); 73-22-3 (Tryptophan); 74-79-3 (Arginine); 9035-37-4 (Cytochrome b); 9064-79-3 (cytochrome b562, E coli)

CN 0 (Genetic Vectors); 0 (Hemerythrin); 0 (Oligodeoxyribonucleotides); 0 (Proteins); 0 (Recombinant Proteins); 0 (Serum Albumin, Bovine); 0 (myohemerythrin)

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(FILE 'HOME' ENTERED AT 13:07:46 ON 09 JUL 2003)  
SET COST OFF

FILE 'HCAPLUS' ENTERED AT 13:07:58 ON 09 JUL 2003

L1 1 S US20020048776/PN  
L2 6 S (WO9726277 OR WO9116683 OR WO9321206 OR US5557535 OR WO930148  
L3 1 S GOEDE ?/AU AND 1997/PY AND (18 AND 9 AND 1113)/SO

FILE 'WPIX' ENTERED AT 13:15:16 ON 09 JUL 2003

L4 6 S (WO9726277 OR US5495423 OR WO9116683 OR WO9321206 OR US555753

FILE 'MEDLINE' ENTERED AT 13:15:36 ON 09 JUL 2003

L5 1 S PREISSNER ?/AU AND 1998/PY AND (280 AND 3 AND 535)/SO

FILE 'WPIX' ENTERED AT 13:16:03 ON 09 JUL 2003

L6 1 S US20020048776/PN  
E FROMMEL C/AU  
L7 3 S E3  
E PREISSNER R/AU  
L8 3 S E3  
E GOEDE A/AU  
L9 4 S E3,E4  
E JERINI/PA  
L10 11 S E3-E7

E FROEMMEL/AU  
 L11 7 S E5  
 L12 1 S L4,L6 AND L7-L11  
 L13 18 S L7-L11 NOT L12  
 L14 7 S L4,L6,L12

FILE 'WPIX' ENTERED AT 13:26:40 ON 09 JUL 2003

FILE 'HCAPLUS' ENTERED AT 13:26:57 ON 09 JUL 2003

E PREISSNER C/AU  
 E PREISSNER R/AU  
 L15 18 S E3,E4  
       E FROMMEL C/AU  
 L16 16 S E3,E5  
       E FROEMMEL C/AU  
 L17 43 S E3,E4  
       E GOEDE A/AU  
 L18 63 S E3-E6,E9,E10  
       E JERINI/PA,CS  
 L19 36 S E3-E22  
 L20 2 S L1-L3 AND L15-L19  
 L21 8 S L1-L3,L20  
 L22 149 S L15-L19 NOT L21  
       E LIGAND/CT  
       E E38+ALL  
 L23 15338 S E1  
 L24 30095 S E1+NT  
 L25 1 S L21 AND L23,L24  
 L26 8 S L21,L25  
 L27 0 S L22 AND L23,L24  
 L28 5 S L22 AND LIGAND  
       E PEISSNER R/AU  
 L29 1 S E4 AND L28  
 L30 5 S L28,L29  
       SEL DN AN 4 5  
 L31 2 S L30 AND E1-E6  
 L32 10 S L26,L31  
 L33 343188 S L23,L24 OR LIGAND  
 L34 101010 S L33 AND (?PEPTIDE? OR ?PROTEIN? OR ENZYM? OR AMINO ACID?)  
 L35 21636 S L33 AND (PEPTIDE? OR PROTEIN? OR ENZYM? OR AMINO ACID?)/SX,SC  
 L36 48827 S L33 AND (PEPTIDE? OR PROTEIN? OR ENZYM? OR AMINO(L)ACID?)/CW  
 L37 103800 S L34-L36  
       E SECONDARY STRUCTURE/CT  
 L38 6956 S E3,E4  
       E E3+ALL  
 L39 24837 S E4,E3+NT  
 L40 1318 S L37 AND L38,L39  
 L41 1021 S L37 AND SECONDARY STRUCTURE  
 L42 1776 S L40,L41  
       E E1+ALL  
 L43 21752 S E2,E3,E1+NT AND L37  
 L44 1601 S L42 AND L43  
 L45 1776 S L42,L44  
       E MOLECULAR SURFACE/CT  
       E E3+ALL  
 L46 367 S E3  
       E E4+ALL  
 L47 322 S E2+NT  
       E E5+ALL  
 L48 4867 S E2+NT  
       E E15+ALL  
       E MOLECULAR SURFACE/CT  
       E E4+ALL

L49           706 S E2  
 L50           14 S L45 AND (L46-L49 OR MOLECULAR SURFACE)  
               SEL DN AN 3 6 10 11 14  
 L51           5 S L50 AND E1-E15  
 L52           32 S L45 AND (PROTEIN SURFACE OR SURFACE AREA)  
 L53           27 S L52 NOT L50  
 L54           1 S L53 AND PROTEIN SURFACE RECOGNITION  
 L55           6 S L51, L54  
               E MOLECULAR RECOGNITION/CT  
               E E3+ALL  
 L56           8689 S E2, E1+NT  
               E E6+ALL  
 L57           80573 S E1+NT  
               E E17+ALL  
 L58           4443 S E4, E3+NT  
               E E15+ALL  
 L59           549 S E2  
 L60           359 S L45 AND L56-L59  
 L61           15 S L60 AND (DRUG SCREENING+NT OR SCREENING+NT OR HIGH THROUGHPUT  
 L62           11 S L60 AND (COMPUTER APPLICATION+NT OR ALGORITHM+NT OR DATABASES  
 L63           18 S L61, L62  
 L64           3 S L32 AND L33-L63  
 L65           14 S L32, L55, L64  
 L66           9 S L65 AND (COMPUTER APPLICATION+NT OR ALGORITHM+NT OR DATABASES  
 L67           14 S L65, L66  
 L68           35 S L45 AND (COMPUTER APPLICATION+NT OR ALGORITHM+NT OR DATABASES  
               E MODEL/CT  
               E E6+ALL  
               E E2+ALL  
               E E2+ALL  
 L69           179 S L45 AND E3-E5, E2+NT  
 L70           25 S L45 AND E39+NT  
 L71           16 S L45 AND E41+NT  
               E MODEL/CT  
               E E6+ALL  
               E E2+ALL  
 L72           208 S L68-L71  
 L73           22 S L72 AND LIGAND?/CW  
 L74           34 S L67, L73  
 L75           23 S L72 AND L74  
 L76           34 S L74, L75  
 L77           21 S L76 AND (PY<=1999 OR PRY<=1999 OR AY<=1999)  
 L78           13 S L76 NOT L77  
 L79           87 S L72 AND (PY<=1999 OR PRY<=1999 OR AY<=1999)  
 L80           76 S L79 NOT L77  
               SEL DN AN 2 23 41 74 75  
 L81           5 S L80 AND E1-E15  
 L82           26 S L77, L81  
 L83           26 S L82 AND L1-L3, L15-L82  
 L84           26 S L83 AND (SCREEN? OR SECOND? OR STRUCTUR? OR MOLECUL? OR SURFA  
 L85           23 S L84 AND (AMINO ACID OR CONFORM? OR FOLD?)  
 L86           26 S L84, L85

FILE 'HCAPLUS' ENTERED AT 14:16:12 ON 09 JUL 2003

FILE 'MEDLINE' ENTERED AT 14:16:42 ON 09 JUL 2003

              E PROTEIN STRUCTURE/CT  
               E E12+ALL  
 L87           32663 S E10+NT  
               E DATABASE/CT  
               E E35+ALL  
 L88           815 S E6+NT AND L87  
 L89           410 S L88 AND PY<=1999

L90 19542 S L87 AND PY<=1999  
 L91 14192 S L1./CT AND L90  
 L92 14192 S L89,L91  
     E MOLECULAR SURFACE/CT  
     E E1+ALL  
 L93 13229 S E8+NT AND L92  
     E E80+ALL  
 L94 4712 S E4+NT AND L92  
 L95 1044 S LIGAND AND L92  
 L96 1018 S L95 AND L93,L94  
     E LIGANDS/CT  
     E E3+ALL  
 L97 476 S E7 AND L90  
 L98 1440 S LIGAND AND L90  
 L99 1440 S L97,L98,L95  
 L100 1359 S L99 AND D12./CT  
 L101 536 S L99 AND D8./CT  
 L102 1433 S L100,L101  
     E CONFORMATION/CT  
     E E8+ALL  
 L103 1433 S L102 AND E2+NT  
     E E2+ALL  
 L104 13 S L103 AND L88  
     SEL DN AN 1 5 7 8 9 11-13  
 L105 8 S L104 AND E1-E24  
     E BINDING SITES/CT  
     E E3+ALL  
 L106 172215 S E4+NT  
     E E26+ALL  
 L107 105279 S E7+NT  
 L108 5586 S L90 AND L106,L107  
 L109 809 S L108 AND L99  
 L110 7 S L109 AND L88  
 L111 594 S L109 AND L93,L94  
 L112 805 S L109 AND L103  
 L113 10 S L105,L110 AND L87-L112  
     E FROMMEL C/AU  
 L114 45 S E3,E4  
     E FROEMMEL C/AU  
 L115 3 S E3,E4  
     E PREISSNER R/AU  
 L116 14 S E3,E4  
     E GOEDE A/AU  
 L117 18 S E3-E8  
 L118 64 S L114-L117  
 L119 17 S L118 AND L87-L113  
     SEL DN AN 2-5 8 10-12  
 L120 8 S E1-E24  
 L121 17 S L113,L120 AND L87-L120  
 L122 56 S L118 NOT L121  
     SEL DN AN 14 22  
 L123 3 S E24-E30  
 L124 19 S L121,L123 AND L87-L123  
 L125 19 S L5,L124